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GENOME ANNOUNCEMENT

Genome Sequence of *Pseudomonas stutzeri* SDM-LAC, a Typical Strain for Studying the Molecular Mechanism of Lactate Utilization

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***Pseudomonas stutzeri* SDM-LAC is an efficient lactate utilizer with various applications in biocatalysis. Here we present a 4.2-Mb assembly of its genome. The annotated four adjacent genes form a lactate utilization operon, which could provide further insights into the molecular mechanism of lactate utilization.**

Pseudomonas stutzeri, which is widely distributed in the environment, was first described by Burri and Stutzer in 1895 (2, 9). Some strains of this species were particularly studied because of their specific functions in nature, such as nitrification, denitrification, degradation of aromatic compounds, and nitrogen fixation (9). *P. stutzeri* SDM-LAC (the strain was previously named SDM, CCTCC no. M206010) has received attention because of its good ability to produce pyruvate by utilizing lactate without hydrogen peroxide production detected (7). Other potential applications of this strain, such as 2-oxobutyrate production (5) and kinetic resolution of 2-hydroxy acid racemic mixtures (4, 6), have also been explored. On the basis of the results of some primary enzymological researches (11), it is thought that the enzymes that participate in lactate utilization are crucial for these applications. Thus, genetic analysis in the strain should be carried out to investigate the molecular mechanism and related key enzymes of lactate utilization.

Here, we present a draft genome sequence of strain SDM-LAC, which was obtained using the Illumina Genome Analyzer IIx system. A total of 3,909,322 filtered reads were assembled into 201 contigs using Velvet algorithms (17). Genome annotation was performed by the RAST server (1). The functional description was determined using the system for delineating clusters of orthologous genes (COG) (14). Genes encoding tRNAs and rRNAs were identified by tRNAscan-SE (10) and RNAmmer (8), respectively.

The draft genome sequence of strain SDM-LAC consists of 4,242,853 bases with a GC content of 60.4%. There are 51 predicted tRNAs in it. A total of 3,884 protein-coding sequences (CDSs) were identified with an average length of 935 bp. The coding percentage is 85.6%, and 2,893 CDSs have functional predictions. Compared with the three other sequenced *P. stutzeri* strains, A1501 (15), DSM 4166 (16), and CGMCC 1.1803 (3), 2,580 (66.4%) CDSs were identified as conserved in all four strains, and 689 (17.7%) CDSs were identified as specific ones in strain SDM-LAC by using the mGenomeSubtractor server (13).

A total of 482 subsystems were determined using the RAST server. Four adjacent genes (*lldR*, *lldP*, *lldD*, and *dld-II*) encoding a lactate-responsive regulator LldR, an L-lactate permease, an L-lactate dehydrogenase, and a predicted D-lactate dehydrogenase, respectively, were annotated in the lactate utilization subsystem. The homolog of the predicted D-lactate dehydrogenase has been proven to belong to a novel family of bacterial D-lactate dehydrogenases (12). These genes form an operon related to lactate utilization (12). The operon is a good model for studying the molecular mechanism of lactate utilization in bacteria. The enzymes encoded by the three putative structural genes (*lldP*, *lldD*, and *dld-II*) may play a key role in the biocatalysis processes mentioned before. However, most of the genes involved in nitrogen fixation in *P. stutzeri* A1501 (15) were not annotated in the strain SDM-LAC genome sequence. Further analysis of the genome sequence might provide other useful information for studying the molecular mechanism of lactate utilization and potential applications in biocatalysis by strain SDM-LAC.

Nucleotide sequence accession numbers. The whole-genome shotgun sequence has been deposited at DDBJ/EMBL/GenBank under accession AGSX00000000. The version described in this paper is the first version, with accession number AGSX01000000.

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